SEQUENCE LISTING

- <110> Batard, Yannick
 Durst, Francis
 Schalk, Michel
 Werck-Reichhart, Daniele
- <120> RECODING OF DNA SEQUENCES PERMITTING EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST

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Leu	Asn	Ala	Glu	Arg	Ser	Ile	Leu	Ser	Gln	Ser	Phe	Asp	Tyr	Asn	Tyr
	210					215					220				
Gly	Asp	Phe	Ile	Pro	Val	Leu	Arg	Pro	Phe		Arg	Arg	Tyr	Leu	
225		_		_	230	1	_	_		235	1	-1	~ 1	3	240
_	Cys	Thr	Asn	Leu 245	Lys	Thr	Lys	Arg	Met 250	Lys	Val	Pne	GIU	255	HIS
	17-1	Gln	Gl n		Lys	Glu	Δla	T.e.ii		Lvg	Thr	Glv	Glu		Ara
# File	vai	GIII	260	Arg	ДуЗ	Olu	AΙα	265	Olu	шуы	1111	O±7	270		••••
Čvs	Ala	Met		His	Ile	Leu	Glu		Glu	Arg	Lys	Gly		Ile	Asn
LÍ		275	•				280				_	285			
Щs	Asp	Asn	Val	Leu	Tyr			Glu	Asn	Ile		Val	Ala	Ala	Ile
	290	· -· -				295					3.00			•	
71	Thr	Thr	Leu	Trp	Ser	Ile	Glu	Trp	Gly		Ala	GLu	Leu	Val	
3 -05	Deep	~ 1	T10	~1 n	310 Gln	Tara	T 011	7 *~	C111	315	Tlo	1727	λls	172 J	320
ms H	Pro	GIU	iie	325	GIII	пув	пеп		330	Giu	116	vaı	ALG	335	пец
	Ala	Glv	Val		Val	Thr	Glu			Leu	Glu	Arq	Leu		Tyr
		1	340					345	•			_	350		-
⊑ Leu	Ģln	Ser	Val	Val	Lys	Glu	Thr	Leu	Arg	Leu	Arg	Met	Ala	Ile	Pro
		355			•		360					365			
Leu		Val	Pro	His	Met		Leu	Ser	Asp	Ala		Leu	Ala	Gly	Tyr
_	370	_		~ 3		375	- 7 -	T	**- 7	7	380	·	Dha	T 011	7.7.
	TTE	Pro	Ala	GIU	Ser 390	ьys	TTE	ьeu	vaı,	395	Ala	пр	PHE	пеп	400
385	Δen	Pro	Lvs	Ara	Trp	Val	Ara	Ala	Asp		Phe	Ara	Pro	Glu	
ASII	лор	110	1375	405					410			5		415	5
Phe	Leu	Glu	Glu		Lys	Ala	Val	Glu		His	Gly	Asn	Asp	Phe	Arg
			420		-			425			_		430		
Phe	Val	Pro	Phe	Gly	Val	Gly	Arg	Arg	Ser	Cys	Pro	Gly	Ile	Ile	Leu
		435					440					445		_	
Ala		Pro	Ile	Ile	Gly		Thr	Leu	Gly	Arg		Val	GIn	Asn	Phe
a 1	450	T	Dec =	Dwa	Dwo	455	C1~	7. ~~	Tura	тіл	460	Thr	ሞኮኍ	درای	Lare
	ьeu	ьeu	PLO		Pro 470	σтλ	GIII	vah	пур	475	vah	TIIT	TIIT	JIU	480
465					¥ / U					4 / J					-00



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490
495

Lys Pro Leu Glu Ala 500

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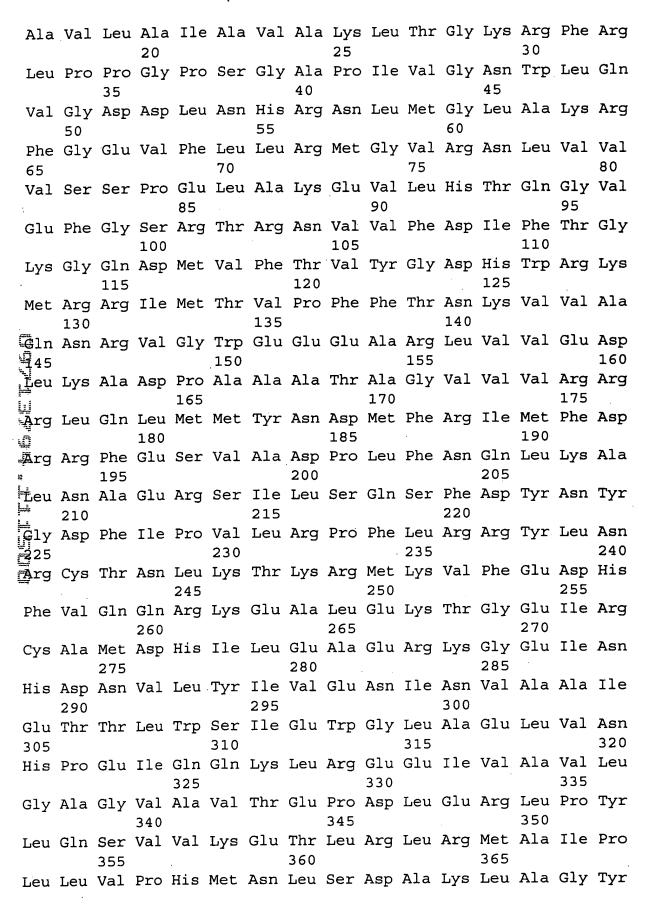
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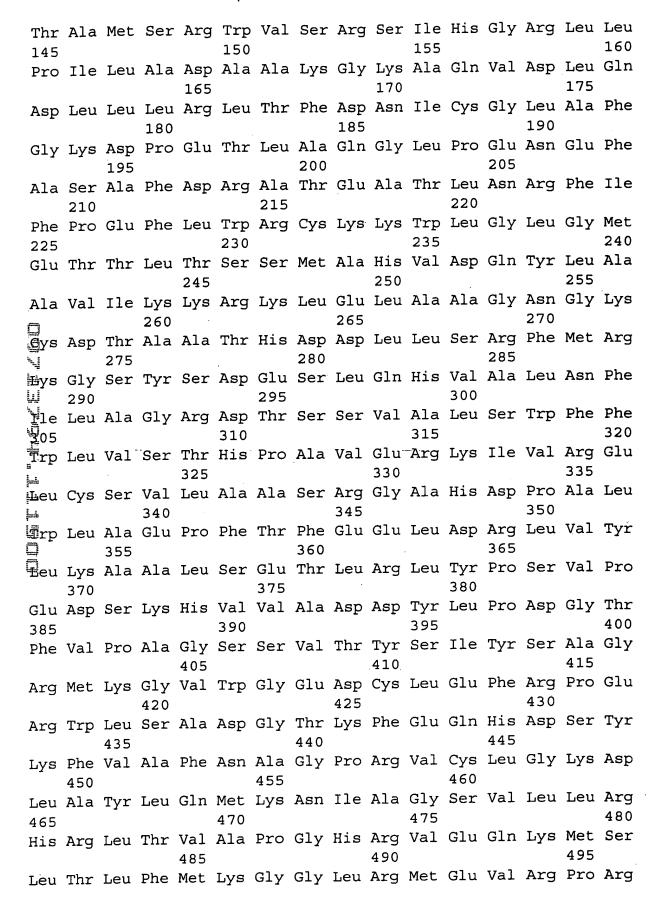
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385					390					395					400
		Pro	īvs	Ara			Ara	Ala	Asp	Glu	Phe	Ara	Pro	Glu	Ara
ASII	пор	120		405					410			5	_	415	5
m1	T	a 1	01. ,			אן א	17-1	Clu			Glw	λen	λen		λνα
Phe	ьeu	GIU			. гув	Ald	vai			UIS	GIY	ASII		Phe	Arg
			420				_	425		_	_		430		_
Phe	Val	Pro	Phe	Gly	Val	GLy			Ser	Cys	Pro		ITe	Ile	Leu
		435					440					445			
Ala	Leu	Pro	Ile	Ile	Gly	Ile	Thr	Leu	Gly	Arg	Leu	Val	Gln	Asn	Phe
	450					455					460				
Gln	Leu	Leu	Pro	Pro	Pro	Gly	Gln	Asp	Lys	Ile	Asp	Thr	Thr	Glu	Lys
465					470					475					480
	Glv	Gln	Phe	Thr	Asn	Gln	Ile	Leu	Lvs	His	Ala	Thr	Ile	Val	Cys
110	011			485					490					495	•
Tara	Dro	T.e.u	Glu	Ala											
_	PIO	пеп		nia											
Ō			500												
	-														
~ <u>.</u> [210>													
		211>													
W Li	<2	212>	PRT		•										
	<2	213>	Art:	ific:	ial S	Sequ	ence								
받															
=======================================	<2	220>													
<u>-</u>	<2	223>	Alte	ered	sequ	ience	es								
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\Box_1	0		1	5	_				10					15	•
******	λla	Trn	Dhe		Δra	Met	Ser	Δτα		T.eu	Ara	Glv	Pro	Arg	Val
Met	ΑΙα	ттр		тър	AI 9	ricc	DCI	25	OLY	ncu.	****9	017	30	9	val
_	D	**- 7	20	α1	Com	T 011	Dwo		T 011	77-7	<i>(</i> 122	цiс		C1,,	7 00
Trp	Pro		Leu	GIY	ser	ьeu		GTA	ьеи	vaı	GIII		AIG	Glu	Asp
		35					40	_	_	_		45	~1	m1	_
Met	His	Glu	Trp	Ile	Ala		Asn	Leu	Arg	Arg		GIY	GIY	Thr	Tyr
	50					55					60				
Gln	Thr	Cys	Ile	Phe	Ala	Val	Pro	Gly	Val	Ala	Arg	Arg	Gly	Gly	Leu
65					70					75					80
	Thr	Val	Thr	Cys	Asp	Pro	Arg	Asn	Leu	Glu	His	Val	Leu	Lys	Ala
				85	-		_		90					95	
λrα	Dhe	Δen	Asn		Pro	Lvs	Glv	Pro		Trp	His	Glv	Val	Phe	Ara
AIG	FIIC	чэр	100	- 7 -		_, _	017	105				1	110		5
	T	T		7 000	C1	Tla	Dho		C02	7 an	Clar	λen		TYD	T.011
Asp	ьеи		стХ	Ash	атй	тте		HSII	SEI	Mph	GIA		TIIL	Trp	ьeu
	_	115	_	1			120	~3	1	m1	m)-	125	տ ե	T	7
Ala	Gln	Arg	Lys	Thr	Ala		Leu	Glu	Phe	Thr		arg	Inr	Leu	Arg
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510 505 500 Asp Leu Ala Pro Val Leu Asp Glu Pro Cys Gly Leu Asp Ala Gly Ala 520 Ala Thr Ala Ala Ala Ser Ala Thr Ala Pro Cys Ala 540 535 530 <210> 20 <211> 541 <212> PRT <213> Artificial Sequence <220> <223> Altered sequences <400> 20 Met Glu Val Gly Thr Trp Ala Val Val Ser Ala Val Ala Ala Tyr 10 Met Ala Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val 20 Prp Pro Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp Met His Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr Gln Thr Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Gly Leu ₩al Thr Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala 90 arg Phe Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu 120 Ala Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg 135 130 Thr Ala Met Ser Arg Trp Val Ser Arg Ser Ile His Gly Arg Leu Leu 150 155 Pro Ile Leu Ala Asp Ala Ala Lys Gly Lys Ala Gln Val Asp Leu Gln 165 Asp Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Ala Phe 185 180 Gly Lys Asp Pro Glu Thr Leu Ala Gln Gly Leu Pro Glu Asn Glu Phe 205 200 Ala Ser Ala Phe Asp Arg Ala Thr Glu Ala Thr Leu Asn Arg Phe Ile 215 Phe Pro Glu Phe Leu Trp Arg Cys Lys Lys Trp Leu Gly Leu Gly Met 235 240 230 225



Glu	Thr	Thr	Leu	Thr 245	Ser	Ser	Met	Ala	His 250	Val	Asp	Gln	Tyr	Leu 255	Ala
			260					265	Leu		,		270		
_		275					280		Leu			285			
Lys	Gly 290	Ser	Tyr	Ser	Asp	Glu 295	Ser	Leu	Gln	His	Val 300	Ala	Leu	Asn	Phe
Ile 305	Leu	Ala	Gly	Arg	Asp 310	Thr	Ser	Ser	Val	Ala 315	Leu	Ser	Trp	Phe	Phe 320
Trp				325		•			Glu 330					335	
k.	_		340					345	Gly				350		
-		355					360		Glu			365			
뎔eu	370					375					380				
Glu 385	_				390					395					400
Phe				405					410					415	
Ārg		_	420		i			425					430		
Ārg		435					440					445			
# ! F	450		·			455			Arg		460				
∄eu 465					470					475					480
				485					Arg 490					495	
			500					505					510		Arg
_		515					520					525	Ala	Gly	Ala
Ala	Thr 530	Ala	Ala	Ala	Ala	Ser 535	Ala	Thr	Ala	Pro	Cys 540	Ala			